



SEQUENCE LISTING

#13
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JUL 25 2001

TECH CENTER 1600/2900

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<120> ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

<130> 50447

<140> US 09/358,321

<141> 1999-07-21

<150> US 60/093,587

<151> 1998-07-21

<160> 60

<170> PatentIn Ver. 2.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5' primer

<220>

<221> unsure

<222> (12)

<223> n can be a,t,g, or c in this degenerate primer

<400> 1

gargaraaym gncaygg

17

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' primer

<220>

<221> unsure

<222> (7)

<223> n can be a,t,g, or c in this degenerate primer

<400> 2

ytcrtgnccky ttytcrtc

18

<210> 3

<211> 276

<212> DNA

<213> Zea mays

<220>
 <221> CDS
 <222> (1)..(276)

<400> 3
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 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr
 1 5 10 15
 ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att 96
 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
 20 25 30
 ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc 144
 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
 35 40 45
 atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac 192
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
 50 55 60
 act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc 240
 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
 65 70 75 80
 tgc ggc atc atc gcc tca gat gag aag cga cat gaa 276
 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
 85 90

<210> 4
 <211> 92
 <212> PRT
 <213> Zea mays

<400> 4
 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr
 1 5 10 15
 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
 20 25 30
 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
 35 40 45
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
 50 55 60
 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
 65 70 75 80
 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
 85 90

<210> 5
 <211> 1621
 <212> DNA
 <213> Zea mays

<400> 5																
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atcccaatct	cgcgaggggca	agcagcaggg	tctgcggcgg	cggcggcggc	cgcgcttccg	120										
gctcccccttc	ccattggcct	ccacg	atg	gcg	ctc	cg	ctc	aac	gac	gtc	gcg	172				
			Met	Ala	Leu	Arg	Leu	Asn	Asp	Val	Ala					
			-30						-25							
ctc	tgc	ctc	tcc	ccg	ccg	ctc	gcc	gcc	cg	cg	cg	cg	cg	agc	agc	220
Leu	Cys	Leu	Ser	Pro	Pro	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Arg	Ser	Ser	
			-20				-15					-10				
ggc	agg	ttc	gtc	gcc	gtc	gcc	tcc	atg	acg	tcc	gcc	gtc	tcc	acc	aag	268
Gly	Arg	Phe	Val	Ala	Val	Ala	Ser	Met	Thr	Ser	Ala	Val	Ser	Thr	Lys	
	-5				-1	1				5					10	
gtc	gag	aat	aag	aag	cca	ttt	gct	cct	cca	agg	gag	gta	cat	gtc	cag	316
Val	Glu	Asn	Lys	Lys	Pro	Phe	Ala	Pro	Pro	Arg	Glu	Val	His	Val	Gln	
				15					20					25		
gtt	aca	cat	tca	atg	cca	cct	cac	aag	att	gaa	att	ttc	aag	tcg	ctt	364
Val	Thr	His	Ser	Met	Pro	Pro	His	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Leu	
			30					35					40			
gat	gat	tgg	gct	aga	gat	aat	atc	ttg	acg	cat	ctc	aag	cca	gtc	gag	412
Asp	Asp	Trp	Ala	Arg	Asp	Asn	Ile	Leu	Thr	His	Leu	Lys	Pro	Val	Glu	
		45					50					55				
aag	tgt	tgg	cag	cca	cag	gat	ttc	ctc	ccg	gac	cca	gca	tct	gaa	gga	460
Lys	Cys	Trp	Gln	Pro	Gln	Asp	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Glu	Gly	
	60					65					70					
ttt	cat	gat	gaa	gtt	aag	gag	ctc	aga	gaa	cgt	gcc	aag	gaa	atc	cct	508
Phe	His	Asp	Glu	Val	Lys	Glu	Leu	Arg	Glu	Arg	Ala	Lys	Glu	Ile	Pro	
	75				80					85					90	
gat	gat	tat	ttt	gtt	tgt	ttg	gtg	gga	gac	atg	att	acc	gag	gaa	gct	556
Asp	Asp	Tyr	Phe	Val	Cys	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	
				95					100				105			
cta	cca	aca	tac	cag	act	atg	ctt	aac	acc	ctc	gac	ggg	gtc	aga	gat	604
Leu	Pro	Thr	Tyr	Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	
			110					115					120			
gag	aca	ggg	gca	agc	ccc	act	gcc	tgg	gct	gtt	tgg	acg	agg	gca	tgg	652
Glu	Thr	Gly	Ala	Ser	Pro	Thr	Ala	Trp	Ala	Val	Trp	Thr	Arg	Ala	Trp	
		125					130					135				
act	gct	gag	gag	aac	agg	cat	ggg	gat	ctg	ctc	aac	aag	tat	atg	tac	700
Thr	Ala	Glu	Glu	Asn	Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Met	Tyr	
	140					145					150					

ctc act ggg agg gtg gat atg agg cag att gag aag aca att cag tat	748
Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr	
155 160 165 170	
ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt	796
Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu	
175 180 185	
ggt ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac	844
Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His	
190 195 200	
ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca	892
Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala	
205 210 215	
caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg	940
Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala	
220 225 230	
tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc	988
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr	
235 240 245 250	
gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc	1036
Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala	
255 260 265	
cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc	1084
His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser	
270 275 280	
atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac	1132
Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp	
285 290 295	
atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt	1180
Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly	
300 305 310	
ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct	1228
Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala	
315 320 325 330	
tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa	1276
Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys	
335 340 345	
gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg	1324
Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu	
350 355 360	
tgagatcgga aacctgctgc ggactgctta gacaagacct gctgtgtctg cgttacatag	1384
gtctccagggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaacgtgtt	1444
ggtctgtggt gtagctttgt ttttattttg tatttttctg ctttgatgta caacctgtgg	1504
ccgcatgaac tggggcggtgg agatgggagc gaccatgccg tactttgtct gtcgctggcg	1564
gtgtgtttcg gtatgttatt tgagttgctc agatctgtta aaaaaaaaaa aaaaaaa	1621

<210> 6
<211> 393
<212> PRT
<213> Zea mays

<400> 6

Met	Ala	Leu	Arg	Leu	Asn	Asp	Val	Ala	Leu	Cys	Leu	Ser	Pro	Pro	Leu	
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Ala	Ala	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Gly	Arg	Phe	Val	Ala	Val	Ala	
-15					-10					-5				-1	1	
Ser	Met	Thr	Ser	Ala	Val	Ser	Thr	Lys	Val	Glu	Asn	Lys	Lys	Pro	Phe	
			5					10					15			
Ala	Pro	Pro	Arg	Glu	Val	His	Val	Gln	Val	Thr	His	Ser	Met	Pro	Pro	
		20					25					30				
His	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Leu	Asp	Asp	Trp	Ala	Arg	Asp	Asn	
	35					40					45					
Ile	Leu	Thr	His	Leu	Lys	Pro	Val	Glu	Lys	Cys	Trp	Gln	Pro	Gln	Asp	
50					55					60					65	
Phe	Leu	Pro	Asp	Pro	Ala	Ser	Glu	Gly	Phe	His	Asp	Glu	Val	Lys	Glu	
				70					75					80		
Leu	Arg	Glu	Arg	Ala	Lys	Glu	Ile	Pro	Asp	Asp	Tyr	Phe	Val	Cys	Leu	
			85					90					95			
Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Met	
		100					105					110				
Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala	Ser	Pro	Thr	
	115					120					125					
Ala	Trp	Ala	Val	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu	Asn	Arg	His	
130					135					140					145	
Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Met	Tyr	Leu	Thr	Gly	Arg	Val	Asp	Met	
				150					155					160		
Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp	
			165					170					175			
Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	Thr	Ser	Phe	
		180					185					190				
Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	Arg	His	Ala	
	195					200					205					
Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly	Ile	Ile	Ala	
210					215					220					225	
Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	Val	Glu	Lys	
				230					235					240		
Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu	Ala	Asp	Met	
			245					250					255			

Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
260 265 270

Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
275 280 285

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
290 295 300 305

Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
310 315 320

Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
325 330 335

Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
340 345 350

Trp Val Tyr Gly Arg Asp Val Gln Leu
355 360

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
atggctagcc tccgcctcaa cgacgtcgcg 30

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
aaagctagct catcacagtt ggacgtccct accgta 36

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
accatggcta gcatgacgtc cgccgtctcc 30

<210> 10
<211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 10
 gatgatgcta gctcacagtt ggacgtccct 30

<210> 11
 <211> 1107
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (4)..(1092)

<400> 11
 acc atg gct acg atg acg tcc gcc gtc tcc acc aag gtc gag aat aag 48
 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys 15
 1 5 10 15
 aag cca ttt gct cct cca agg gag gta cat gtc cag gtt aca cat tca 96
 Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser 30
 20 25 30
 atg cca cct cac aag att gaa att ttc aag tcg ctt gat gat tgg gct 144
 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala 45
 35 40 45
 aga gat aat atc ttg acg cat ctc aag cca gtc gag aag tgt tgg cag 192
 Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln 60
 50 55 60
 cca cag gat ttc ctc ccg gac cca gca tct gaa gga ttt cat gat gaa 240
 Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu 75
 65 70 75
 gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct gat gat tat ttt 288
 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe 95
 80 85 90 95
 gtt tgt ttg gtg gga gac atg att acc gag gaa gct cta cca aca tac 336
 Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr 110
 100 105 110
 cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca 384
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala 125
 115 120 125
 agc ccc act gcc tgg gct gtt tgg acg agg gca tgg act gct gag gag 432
 Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu 140
 130 135 140
 aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act ggg agg 480
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg 155
 145 150 155
 gtg gat atg agg cag att gag aag aca att cag tat ctt att ggc tct 528

Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser		
160					165					170					175		
gga	atg	gat	cct	agg	act	gag	aat	aat	cct	tat	ctt	ggt	ttc	atc	tac	576	
Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr		
				180					185					190			
acc	tcc	ttc	caa	gag	cgg	gcg	acc	ttc	atc	tca	cac	ggg	aac	act	gct	624	
Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala		
			195					200					205				
cgt	cac	gcc	aag	gac	ttt	ggc	gac	tta	aag	ctt	gca	caa	atc	tgc	ggc	672	
Arg	His	Ala	Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly		
		210					215					220					
atc	atc	gcc	tca	gat	gag	aag	cga	cat	gaa	act	gcg	tac	acc	aag	atc	720	
Ile	Ile	Ala	Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile		
	225					230					235						
gtg	gag	aag	ctg	ttt	gag	atc	gac	cct	gat	ggt	acc	gtg	gtc	gct	ctg	768	
Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu		
240					245					250					255		
gct	gac	atg	atg	agg	aag	aag	atc	tca	atg	cct	gcc	cac	ctg	atg	ttt	816	
Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	Ala	His	Leu	Met	Phe		
				260					265					270			
gac	ggg	cag	gac	gac	aag	ctg	ttc	gag	cac	ttc	tcc	atg	gtc	gcg	cag	864	
Asp	Gly	Gln	Asp	Asp	Lys	Leu	Phe	Glu	His	Phe	Ser	Met	Val	Ala	Gln		
			275					280					285				
agg	ctt	ggc	gtt	tac	acc	gcc	agg	gac	tac	gcc	gac	atc	ctc	gag	ttc	912	
Arg	Leu	Gly	Val	Tyr	Thr	Ala	Arg	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe		
		290					295					300					
ctc	gtc	gac	agg	tgg	aag	gtg	gcg	agc	ctg	act	ggt	ctg	tcg	ggt	gaa	960	
Leu	Val	Asp	Arg	Trp	Lys	Val	Ala	Ser	Leu	Thr	Gly	Leu	Ser	Gly	Glu		
	305					310					315						
ggg	aac	aag	gcg	cag	gac	tac	ctt	tgc	acc	ctt	gct	tca	aga	atc	agg	1008	
Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Thr	Leu	Ala	Ser	Arg	Ile	Arg		
320					325					330					335		
agg	ctg	gag	gag	agg	gcc	cag	agc	aga	gcc	aag	aaa	gcc	ggc	acg	ctg	1056	
Arg	Leu	Glu	Glu	Arg	Ala	Gln	Ser	Arg	Ala	Lys	Lys	Ala	Gly	Thr	Leu		
				340					345					350			
cct	ttc	agc	tgg	gta	tac	ggt	agg	gac	gtc	caa	ctg	tgagctagca	tcac			1107	
Pro	Phe	Ser	Trp	Val	Tyr	Gly	Arg	Asp	Val	Gln	Leu						
			355					360									

<210> 12
 <211> 363
 <212> PRT
 <213> Zea mays

<400> 12
 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys
 1 5 10 15

Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met
 20 25 30
 Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg
 35 40 45
 Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro
 50 55 60
 Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val
 65 70 75 80
 Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val
 85 90 95
 Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln
 100 105 110
 Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser
 115 120 125
 Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn
 130 135 140
 Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val
 145 150 155 160
 Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly
 165 170 175
 Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr
 180 185 190
 Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg
 195 200 205
 His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile
 210 215 220
 Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val
 225 230 235 240
 Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala
 245 250 255
 Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp
 260 265 270
 Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg
 275 280 285
 Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu
 290 295 300
 Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly
 305 310 315 320
 Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg
 325 330 335
 Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro

<220>
 <223> Description of Artificial Sequence:primer

 <400> 17
 aaagctagcc tsctgcygyt ctkkttwycw ggtryc 36

 <210> 18
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 18
 tacgttacct gagcggccgc gctgggctca agttttttgt ccaccg 46

 <210> 19
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 19
 ttgctagct tactaacact cattcctgtt gaagctct 38

 <210> 20
 <211> 102
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 20
 gcactaggtc aatctagaat ggtaagcgct attgttttat atgtgctttt ggcggcggcg 60
 cattctgcct ttgcggcggt tgtgatgacc ccaaaccac tc 102

 <210> 21
 <211> 738
 <212> DNA
 <213> mouse

 <220>
 <221> unsure
 <222> (16)..(21)
 <223> not known

 <220>
 <221> unsure
 <222> (26)
 <223> not known

 <220>

<221> unsure
 <222> (32)
 <223> not known

<220>
 <221> CDS
 <222> (37)..(693)

<400> 21

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Asp Val Val Met Thr Pro	
1 5	
aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	102
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
10 15 20	
tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta	150
Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu	
25 30 35	
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	198
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr	
40 45 50	
aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt	246
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser	
55 60 65 70	
gga tca ggg aca gat ttc aca ctc aag atc aac aga gtg gag gct gag	294
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Asn Arg Val Glu Ala Glu	
75 80 85	
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg	342
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr	
90 95 100	
ttc gga ggg ggg acc aag ctg gaa ata aaa cgg gct gat gct gca cca	390
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro	
105 110 115	
act gta tcc atc ttc cca cca tcc agt gag cag tta aca tct gga ggt	438
Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly	
120 125 130	
gcc tca gtc gtg tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat	486
Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn	
135 140 145 150	
gtc aag tgg aag att gat ggc agt gaa cga caa aat ggc gtc ctg aac	534
Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn	
155 160 165	
agt tgg act gat cag gac acc aaa gac agc acc tac agc atg agc agc	582
Ser Trp Thr Asp Gln Asp Thr Lys Asp Ser Thr Tyr Ser Met Ser Ser	
170 175 180	
acc ctc acg ttg acc aag gac gag tat gaa cga cat aac agc tat acc	630
Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr	
185 190 195	

tgt gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc	678
Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe	
200 205 210	

aac agg aat gag tgt tagtaagcta gcacgcccga tgggtgggacg gtatgaataa	733
Asn Arg Asn Glu Cys	
215	

tccgg	738
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<210> 22
 <211> 336
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(336)

<400> 22	
gat gtt gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga	48
Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly	
1 5 10 15	

gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	

aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	

cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	

gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

aac aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt	288
Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser	
85 90 95	

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	336
Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105 110	

<210> 23
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 23	
gcactaggtc aatctagaat ggtaagcgct attgttttat atgtgctttt ggcggcggcg	60

gcgcattctg cctttgcggc ggttcaactg cagcagctctg gggctgag

108

<210> 24
<211> 882
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (25)..(837)

<220>
<221> mat_peptide
<222> (79)..(837)

<400> 24

ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
Met Thr Ile Leu Cys Trp Leu Ala Leu
-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat 195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His
25 30 35

tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa 243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
40 45 50 55

gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
60 65 70

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
75 80 85

ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc 387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
90 95 100

gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc 435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly
105 110 115

aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag 483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln
120 125 130 135

cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc 531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser
140 145 150

tgc aag gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
cat cat cat cat cat cat tagggcctct ctggccgatc ccccgaaattt	867
His His His His His	
250	
ccccgatcgt tcaaa	882
<210> 25	
<211> 339	
<212> DNA	
<213> mouse	
<220>	
<221> CDS	
<222> (1) .. (339)	
<400> 25	
cag gtt gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga	48
Gln Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly	
1 5 10 15	
gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	
aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

agc	aga	gtg	gag	gct	gag	gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	288
Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	
			85						90					95		

aca	cat	gtt	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	336
Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
			100					105					110			

ggc																339
Gly																

<210> 26
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 26
 cccggggttg gattcggagc cagatcctga ggatttacc tctgcagaga cagtgaccag 60
 agtc 64

<210> 27
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 27
 gagggtaa cctcaggatc tggctccgaa tccaaaccg gggatgttgt gatgacccca 60
 aac 63

<210> 28
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 28
 gcactaggtc aagcggccgc ttactaattc agatcctctt ctgagatgag tttttcttct 60
 tttatttcca gcttggtc 78

<210> 29
 <211> 459
 <212> DNA
 <213> mouse

<220>

<221> CDS
<222> (19)..(459)

<220>
<221> mat_peptide
<222> (79)..(459)

<400> 29
gcactagggtc aatctaga atg gta agc gct att gtt tta tat gtg ctt ttg 51
Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu
-20 -15 -10

gcg gcg gcg gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct 99
Ala Ala Ala Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser
-5 -1 1 5

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag 147
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
10 15 20

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg cag 195
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln
25 30 35

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act 243
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
40 45 50 55

ggg ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act 291
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
60 65 70

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca 339
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
75 80 85

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg 387
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
90 95 100

ggc caa ggg act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga 435
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly
105 110 115

tct ggc tcc gaa tcc aaa ccc ggg 459
Ser Gly Ser Glu Ser Lys Pro Gly
120 125

<210> 30
<211> 438
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1)..(408)

<400> 30
gag ggt aaa tcc tca gga tct ggc tcc gaa tcc aaa ccc ggg gat gtt 48
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Pro Gly Asp Val

1	5	10	15	
gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga gat caa				96
Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln				
	20	25	30	
gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt aat gga				144
Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly				
	35	40	45	
atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aag				192
Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys				
	50	55	60	
ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg				240
Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg				
	65	70	75	80
ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga				288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg				
	85	90	95	
gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat				336
Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His				
	100	105	110	
gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gaa gaa				384
Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu Glu				
	115	120	125	
aaa ctc atc tca gaa gag gat ctg aattagtaag gggccgcctt gacctagtgc				438
Lys Leu Ile Ser Glu Glu Asp Leu				
	130	135		

<210> 31
 <211> 830
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (7)..(813)

<220>
 <221> mat_peptide
 <222> (67)..(813)

<400> 31	
tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg	48
Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala	
-20 -15 -10	
gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu	
-5 -1 1 5 10	
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc	144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly	
15 20 25	

tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga tct ggc tcc	432
Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser	
110 115 120	
gaa tcc aaa ccc ggg gat gtt gtg atg acc cca aac cca ctc tcc ctg	480
Glu Ser Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu	
125 130 135	
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag	528
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln	
140 145 150	
agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac ctg cag	576
Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln	
155 160 165 170	
aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga	624
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg	
175 180 185	
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat	672
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
190 195 200	
ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat	720
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr	
205 210 215	
ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc	768
Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr	
220 225 230	
aag ctg gaa ata aaa gaa gaa aaa ctc atc tca gaa gag gat ctg	813
Lys Leu Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu	
235 240 245	
aattagtaag cggccgc	830

<210> 32
<211> 269

<212> PRT
<213> mouse

<400> 32

Met	Val	Ser	Ala	Ile	Val	Leu	Tyr	Val	Leu	Leu	Ala	Ala	Ala	Ala	His	
-20					-15					-10					-5	
Ser	Ala	Phe	Ala	Ala	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	
			-1	1				5					10			
Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	
		15					20					25				
Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp	Val	Arg	Gln	Thr	Pro	Val	His	Gly	
	30					35					40					
Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	
45					50					55					60	
Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	
				65					70					75		
Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	
			80					85					90			
Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	
	95						100					105				
Val	Thr	Val	Ser	Ala	Glu	Gly	Lys	Ser	Ser	Gly	Ser	Gly	Ser	Glu	Ser	
	110					115						120				
Lys	Pro	Gly	Asp	Val	Val	Met	Thr	Pro	Asn	Pro	Leu	Ser	Leu	Pro	Val	
125					130					135					140	
Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	
				145					150					155		
Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	
			160					165					170			
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	
		175					180						185			
Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
	190					195						200				
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	
205					210					215					220	
Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	
				225					230					235		
Glu	Ile	Lys	Glu	Glu	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu				
			240					245								

<210> 33
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:c-myc tag

 <400> 33
 gaagaaaaac tcatctcaga agaggatctg 30

 <210> 34
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:p67 leader

 <400> 34
 atggtaagcg ctattgtttt atatgtgctt ttggcggcgg cggcgcatc tgcctttgcg 60

 <210> 35
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 35
 gcactaggtc aatctagaat gactatcctt tgctggctgg cccttctgtc aactctgact 60
 gccgtcaacg ctgcggttgt gatg 84

 <210> 36
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 36
 gcccttggtg ccctcgccgc tgcccggctt gccgctgccg ctggtgctgc cttttatttc 60
 cagcttggtc 70

 <210> 37
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 37
 ggcagcacca gcggcagcgg caagccgggc agcggcgagg gcagcaccaa gggccagggtt 60
 caactgcagc agtc 74

<210> 38
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 38
gcactaggctc aagcggccgc atgatgatga tgatgatgag aaccccgcat tgcagagaca 60
gtgaccagag tc 72

<210> 39
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 39
aaaatttgcg gccgcctaata gatgatgatg atgatgagaa c 41

<210> 40
<211> 462
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (19)..(462)

<220>
<221> mat_peptide
<222> (73)..(462)

<400> 40
gcactaggctc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca 51
Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
-15 -10

act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
-5 -1 1 5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
10 15 20 25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
30 35 40

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
45 50 55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291

Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly		
		60					65					70					
aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	gat	ctg	gga	339	
Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly		
	75					80				85							
gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	ttc	gga	ggg	387	
Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly		
90					95					100				105			
ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	ggc	aag	ccg	435	
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro		
				110					115					120			
ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc								462	
Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly									
			125					130									
 <210> 41																	
<211> 443																	
<212> DNA																	
<213> mouse																	
 <220>																	
<221> CDS																	
<222> (1) .. (423)																	
 <400> 41																	
ggc	agc	acc	agc	ggc	agc	ggc	aag	ccg	ggc	agc	ggc	gag	ggc	agc	acc	48	
Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr		
1				5					10					15			
aag	ggc	cat	gtt	caa	ctg	cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	96	
Lys	Gly	His	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro		
			20					25					30				
ggg	gct	tca	gtg	acg	ctg	tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	144	
Gly	Ala	Ser	Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr		
		35					40					45					
gac	tat	gaa	ata	cac	tgg	gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	192	
Asp	Tyr	Glu	Ile	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu		
	50					55					60						
tgg	att	gga	gct	att	gat	cct	gaa	act	ggg	ggg	act	gcc	tac	aat	cag	240	
Trp	Ile	Gly	Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln		
65					70					75					80		
aag	ttc	aag	gac	aag	gcc	ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	288	
Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr		
				85					90					95			
gcc	tac	atg	gag	ctc	cgc	agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	336	
Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr		
			100					105					110				
tac	tat	aca	aga	tgg	ttt	gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	384	
Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr		
		115					120					125					

gtc tct gca atg cgg ggt tct cat cat cat cat cat cat gcgccgctt	433
Val Ser Ala Met Arg Gly Ser His His His His His His	
130 135 140	

gacctagtgc 443

<210> 42
 <211> 851
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (19)..(831)

<220>
 <221> mat_peptide
 <222> (73)..(831)

<400> 42	
gcactaggctc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca	51
Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser	
-15 -10	

act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc	99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu	
-5 -1 1 5	

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct	147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser	
10 15 20 25	

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac	195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr	
30 35 40	

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc	243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser	
45 50 55	

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg	291
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly	
60 65 70	

aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga	339
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly	
75 80 85	

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg	387
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly	
90 95 100 105	

ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg	435
Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro	
110 115 120	

ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag tct	483
Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln Ser	
125 130 135	

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag	531
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys	
140 145 150	
gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg aag cag	579
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Lys Gln	
155 160 165	
aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act	627
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr	
170 175 180 185	
ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act	675
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr	
190 195 200	
gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca	723
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr	
205 210 215	
tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg	771
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp	
220 225 230	
ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat cat	819
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His His	
235 240 245	
cat cat cat cat gcggccgctt gacctagtgc	851
His His His His	
250	

<210> 43
 <211> 867
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (31)..(843)

<220>
 <221> mat_peptide
 <222> (85)..(843)

<400> 43	
aatttaaacg gatcccgggt accttctaga atg act atc ctt tgc tgg cta gcc	54
Met Thr Ile Leu Cys Trp Leu Ala	
-15	

ctt ctg tca act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca	102
Leu Leu Ser Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro	
-10 -5 -1 1 5	

aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	150
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
10 15 20	

tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta	198
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Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	
		25					30					35				
cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	246
His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	
	40					45					50					
aaa	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	294
Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	
	55				60					65					70	
gga	tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	342
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	
				75					80					85		
gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	390
Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	
			90					95					100			
ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	438
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	
		105					110					115				
ggc	aag	ccg	ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc	cat	gtt	caa	ctg	486
Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	His	Val	Gln	Leu	
	120					125					130					
cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	gtg	acg	ctg	534
Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu	
					140					145					150	
tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	ata	cac	tgg	582
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp	
				155					160					165		
gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	gct	att	gat	630
Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp	
			170					175					180			
cct	gaa	act	ggg	ggg	act	gcc	tac	aat	cag	aag	ttc	aag	gac	aag	gcc	678
Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	
		185					190					195				
ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	726
Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	
	200					205					210					
agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	774
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe	
	215				220					225					230	
gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggg	822
Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly	
				235				240						245		
tct	cat	cat	cat	cat	cat	cat	cat	taggcggccg	ctgcagatct	gatc						867
Ser	His	His	His	His	His	His										
			250													

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<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 44
tttaaaggcc atattggcca tgactatcct ttgctggct 39

<210> 45
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 45
tttaaaggcc atattggcca tggatgttgt gatgacccca aac 43

<210> 46
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 46
tttaaaggcc agagaggccc taatgatgat gatgatgatg agaaccccg c attg 54

<210> 47
<211> 882
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (25)..(837)

<220>
<221> mat_peptide
<222> (79)..(837)

<400> 47
ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
Met Thr Ile Leu Cys Trp Leu Ala Leu
-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

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aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat	195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His	
25 30 35	
tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa	243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys	
40 45 50 55	
gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga	291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
60 65 70	
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat	339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp	
75 80 85	
ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	
tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
cat cat cat cat cat cat tagggcctct ctggccgatc ccccgaattt	867
His His His His His His	
250	
ccccgatcgt tcaaa	882

<210> 48
 <211> 846
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (25)..(786)

<400> 48

ctgcagggtta cggccatatt ggcc atg gat gtt gtg atg acc cca aac cca	51
Met Asp Val Val Met Thr Pro Asn Pro	
1 5	
ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga	99
Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg	
10 15 20 25	
tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg	147
Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp	
30 35 40	
tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt	195
Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val	
45 50 55	
tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca	243
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser	
60 65 70	
ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg	291
Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu	
75 80 85	
gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga	339
Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly	
90 95 100 105	
ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag	387
Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys	
110 115 120	
ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag	435
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln	
125 130 135	
tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc	483
Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys	
140 145 150	
aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg	531
Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg	
155 160 165	
cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa	579
Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu	
170 175 180 185	
act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg	627

Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val	
				190					195					200		
act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	agc	ctg	675
Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	
			205					210					215			
aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	gag	gac	723
Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp	
		220					225					230				
tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggg	tct	cat	771
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly	Ser	His	
	235					240					245					
cat	cat	cat	cat	cat	tagggcctct	ctggccgatc	ccccgaattt	ccccgatcgt								826
His	His	His	His	His												
					250											
tcaaacattt	ggcaataaag															846

<210> 49
 <211> 738
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (19)..(687)
 <223> mature peptide is coded by nucleotides 49 to 687

<400> 49																
cccgggtacc	cttctaga	ctc	gtg	aca	gtt	gtt	gat	ggg	gcc	caa	tcc	cag				51
		Leu	Val	Thr	Val	Val	Asp	Gly	Ala	Gln	Ser	Gln				
			1			5					10					
gtt	caa	ctg	cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	99
Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	
			15					20					25			
gtg	acg	ctg	tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	147
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	
		30				35					40					
ata	cac	tgg	gtg	agg	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	195
Ile	His	Trp	Val	Arg	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	
	45					50					55					
gct	att	gat	cct	gaa	act	ggg	ggg	act	gcc	tac	aat	cag	aag	ttc	aag	243
Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	
	60				65				70							
gac	aag	gcc	ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	291
Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	
				80					85					90		
gag	ctc	cgc	agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	339
Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	
			95					100					105			

aga	tgg	ttt	gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	387
Arg	Trp	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	
		110					115					120				

gcc	aaa	aca	aca	ccc	cca	tca	gtc	tat	cca	ctg	gcc	cct	ggg	tgt	gga	435
Ala	Lys	Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Cys	Gly	
	125					130					135					

gat	aca	act	ggg	tcc	tct	gtg	act	ctg	gga	tgc	ctg	gtc	aag	ggc	tac	483
Asp	Thr	Thr	Gly	Ser	Ser	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	
140					145					150					155	

ttc	cct	gag	tca	gtg	act	gtg	act	tgg	aac	tct	gga	tcc	ctg	tcc	agc	531
Phe	Pro	Glu	Ser	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	
				160					165						170	

agt	gtg	cac	acc	ttc	cca	gct	ctc	ctg	cag	tct	gga	ctc	tac	act	atg	579
Ser	Val	His	Thr	Phe	Pro	Ala	Leu	Leu	Gln	Ser	Gly	Leu	Tyr	Thr	Met	
			175					180					185			

agc	agc	tca	gtg	act	gtc	ccc	tcc	agc	acc	tgg	cca	agt	cag	acc	gtc	627
Ser	Ser	Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Gln	Thr	Val	
		190					195					200				

acc	tgc	agc	gtt	gct	cac	cca	gcc	agc	agc	acc	acg	gtg	gac	aaa	aaa	675
Thr	Cys	Ser	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Thr	Val	Asp	Lys	Lys	
	205					210					215					

ctt	gag	ccc	agc	gcggccgctg	caggtcttga	tcctttcctg	ggacccggca	727
Leu	Glu	Pro	Ser					
220								

agaaccaaaa a	738
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<210> 50
 <211> 42
 <212> DNA
 <213> mouse

<400> 50 gcactaggtc aagcggccgc ttactaacac tcattcctgt tg	42
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<210> 51
 <211> 753
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (7)..(705)

<220>
 <221> mat_peptide
 <222> (67)..(705)

<400> 51 tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala -20 -15 -10	48
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gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu	
-5 -1 1 5 10	
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc	144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly	
15 20 25	
tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gcc aaa aca aca ccc cca tca gtc tat	432
Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr	
110 115 120	
cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg	480
Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu	
125 130 135	
gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg	528
Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp	
140 145 150	
aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg	576
Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu	
155 160 165 170	
cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc	624
Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser	
175 180 185	
acc tgg acc tgc agc gtt gct cac cca gcc agc agc cca agt cag acc	672
Thr Trp Thr Cys Ser Val Ala His Pro Ala Ser Ser Pro Ser Gln Thr	
190 195 200	
gtc acc acg gtg gac aaa aaa ctt gag ccc agc tagtaatgag cggccgctgc	725
Val Thr Thr Val Asp Lys Lys Leu Glu Pro Ser	
205 210	
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<220>
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<220>
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